Harvard
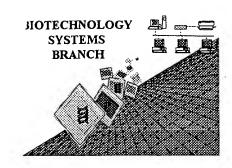
RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: _09/037,657_

Art Unit / Team No. : _1646_

Date Processed by STIC: _6/30/99_

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

F. Hamud

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│   This Raw Listing contains the General Information   │
│   Section and up to first 5 pages.   │
└───┘

```
 1   <110> APPLICANT: Hilton, Douglas J.
 2         Nicola, Nicos A.
 3         Farley, Alison
 4         Wilson, Tracy
 5         Zhang, Jian-Guo
 6         Alexander, Warren
 7         Rakar, Steven                     Does Not Comply
 8         Fabri, Louis                Corrected Diskette Needed
 9         Kojima, Tetsuo
10         Maeda, Masatsugu
11         Kikuchi, Yasufumi
12         Nash, Andrew
13   <120> TITLE OF INVENTION: A NOVEL HAEMPOIETIN RECEPTOR AND GENETIC SEQUENCES
14         ENCODING SAME
15   <130> FILE REFERENCE: DAVIES COLLISON CAVE (CIP)
16   <140> CURRENT APPLICATION NUMBER: US/09/037,657
17   <141> CURRENT FILING DATE: 1998-03-10
18   <150> EARLIER APPLICATION NUMBER: 08/928,720
19   <151> EARLIER FILING DATE: 1997-09-11
20   <160> NUMBER OF SEQ ID NOS: 54
21   <170> SOFTWARE: PatentIn Ver. 2.0
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24   <212> TYPE: PRT
25   <213> ORGANISM: Unknown
26   <220> FEATURE:
27   <221> NAME/KEY: UNSURE
28   <222> LOCATION: (3)
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32           1                 5
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35   <212> TYPE: DNA
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52   <213> ORGANISM: Artificial Sequence
53   <220> FEATURE:
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94   <211> LENGTH: 15
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144    <220> FEATURE:
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149   ccc atg ccc gcg ggt cgc ccg ggc ccc gtc gcc caa tcc gcg cgg cgg   168
150   Met Pro Ala Gly Arg Pro Gly Pro Val Ala Gln Ser Ala Arg Arg
151   1   5   10   15
152   ccg ccg cgg ccg ctg tcc tcg ctg tgg tcg cct ctg ttg ctc tgt gtc   216
153   Pro Pro Arg Pro Leu Ser Ser Leu Trp Ser Pro Leu Leu Leu Cys Val
154   20   25   30
155   ctc ggg gtg cct cgg ggc gga tcg gga gcc cac aca gct gta atc agc   264
156   Leu Gly Val Pro Arg Gly Gly Ser Gly Ala His Thr Ala Val Ile Ser
157   35   40   45
158   ccc cag gac ccc acc ctt ctc atc ggc tcc tcc ctg caa gct acc tgc   312
159   Pro Gln Asp Pro Thr Leu Leu Ile Gly Ser Ser Leu Gln Ala Thr Cys
160   50   55   60
161   tct ata cat gga gac aca cct ggg gcc acc gct gag ggg ctc tac tgg   360
162   Ser Ile His Gly Asp Thr Pro Gly Ala Thr Ala Glu Gly Leu Tyr Trp
163   65   70   75
164   acc ctc aat ggt cgc cgc ctg ccc tct gag ctg tcc cgc ctc ctt aac   408
165   Thr Leu Asn Gly Arg Arg Leu Pro Ser Glu Leu Ser Arg Leu Leu Asn
166   80   85   90   95
167   acc tcc acc ctg gcc ctg gcc ctg gct aac ctt aat ggg tcc agg cag   456
168   Thr Ser Thr Leu Ala Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln
169   100   105   110
170   cag tca gga gac aat ctg gtg tgt cac gcc cga gac ggc agc att ctg   504
171   Gln Ser Gly Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu
172   115   120   125
173   gct ggc tcc tgc ctc tat gtt ggc ttg ccc cct gag aag ccc ttt aac   552
174   Ala Gly Ser Cys Leu Tyr Val Gly Leu Pro Pro Glu Lys Pro Phe Asn
175   130   135   140
176   atc agc tgc tgg tcc cgg aac atg aag gat ctc acg tgc cgc tgg aca   600
177   Ile Ser Cys Trp Ser Arg Asn Met Lys Asp Leu Thr Cys Arg Trp Thr
178   145   150   155
179   ccg ggt gca cac ggg gag aca ttc tta cat acc aac tac tcc ctc aag   648
180   Pro Gly Ala His Gly Glu Thr Phe Leu His Thr Asn Tyr Ser Leu Lys
181   160   165   170   175
182   tac aag ctg agg tgg tac ggt cag gat aac aca tgt gag gag tac cac   696
183   Tyr Lys Leu Arg Trp Tyr Gly Gln Asp Asn Thr Cys Glu Glu Tyr His
184   180   185   190
185   act gtg ggc cct cac tca tgc cat atc ccc aag gac ctg gcc ctc ttc   744
186   Thr Val Gly Pro His Ser Cys His Ile Pro Lys Asp Leu Ala Leu Phe
187   195   200   205
188   act ccc tat gag atc tgg gtg gaa gcc acc aat cgc cta ggc tca gca   792
189   Thr Pro Tyr Glu Ile Trp Val Glu Ala Thr Asn Arg Leu Gly Ser Ala
190   210   215   220
191   aga tct gat gtc ctc aca ctg gat gtc ctg gac gtg gtg acc acg gac   840
192   Arg Ser Asp Val Leu Thr Leu Asp Val Leu Asp Val Val Thr Thr Asp
193   225   230   235
194   ccc cca ccc gac gtg cac gtg agc cgc gtt ggg ggc ctg gag gac cag   888

195	Pro Pro Pro Asp Val His Val Ser Arg Val Gly Gly Leu Glu Asp Gln	
196	240 245 250 255	
197	ctg agt gtg cgc tgg gtc tca cca cca gct ctc aag gat ttc ctc ttc	936
198	Leu Ser Val Arg Trp Val Ser Pro Pro Ala Leu Lys Asp Phe Leu Phe	
199	260 265 270	
200	caa gcc aag tac cag atc cgc tac cgc gtg gag gac agc gtg gac tgg	984
201	Gln Ala Lys Tyr Gln Ile Arg Tyr Arg Val Glu Asp Ser Val Asp Trp	
202	275 280 285	
203	aag gtg gtg gat gac gtc agc aac cag acc tcc tgc cgt ctc gcg ggc	1032
204	Lys Val Val Asp Asp Val Ser Asn Gln Thr Ser Cys Arg Leu Ala Gly	
205	290 295 300	
206	ctg aag ccc ggc acc gtt tac ttc gtc caa gtg cgt tgt aac cca ttc	1080
207	Leu Lys Pro Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe	
208	305 310 315	
209	ggg atc tat ggg tcg aaa aag gcg gga atc tgg agc gag tgg agc cac	1128
210	Gly Ile Tyr Gly Ser Lys Lys Ala Gly Ile Trp Ser Glu Trp Ser His	
211	320 325 330 335	
212	ccc acc gct gcc tcc acc cct cga agt gag cgc ccg ggc ccg ggc ggc	1176
213	Pro Thr Ala Ala Ser Thr Pro Arg Ser Glu Arg Pro Gly Pro Gly Gly	
214	340 345 350	
215	ggg gtg tgc gag ccg cgg ggc ggc gag ccc agc tcg ggc ccg gtg cgg	1224
216	Gly Val Cys Glu Pro Arg Gly Gly Glu Pro Ser Ser Gly Pro Val Arg	
217	355 360 365	
218	cgc gag ctc aag cag ttc ctc ggc tgg ctc aag aag cac gca tac tgc	1272
219	Arg Glu Leu Lys Gln Phe Leu Gly Trp Leu Lys Lys His Ala Tyr Cys	
220	370 375 380	
221	tcg aac ctt agt ttc cgc ctg tac gac cag tgg cgt gct tgg atg cag	1320
222	Ser Asn Leu Ser Phe Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln	
223	385 390 395	
224	aag tca cac aag acc cga aac cag gtc ctg ccg gct aaa ctc	1362
225	Lys Ser His Lys Thr Arg Asn Gln Val Leu Pro Ala Lys Leu	
226	400 405 410	
227	taaggatagg ccatcctcct gctgggtcag acctggaggc tcacctgaat tggagcccct	1422
228	ctgtaccatc tgggcaacaa agaaacctac cagaggctgg ggcacaatga gctcccacaa	1482
229	ccacagcttt ggtccacatg atggtcacac ttggatatac cccagtgtgg gtaaggttgg	1542
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231	aaaaaaaaaa aaaaaaaaaa aaaaaaa	1629
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240	1 5 10 15	
241	Pro Arg Pro Leu Ser Ser Leu Trp Ser Pro Leu Leu Leu Cys Val Leu	
242	20 25 30	
243	Gly Val Pro Arg Gly Gly Ser Gly Ala His Thr Ala Val Ile Ser Pro	
	35 40 45	

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220> to
<223> fields of each sequence which presents at least one n or Xaa.

Line	?	Error/Warning	Original Text
31	W	"N" or "Xaa" used: Feature required	Trp Ser Xaa Trp Ser
1030	W	"N" or "Xaa" used: Feature required	Leu Arg Leu Val Arg Ser Glu Xaa His Met X
1034	W	"N" or "Xaa" used: Feature required	Leu Xaa Asp Leu Gly Gly Ser His Gln Ser P
1036	W	"N" or "Xaa" used: Feature required	Xaa Cys Pro His Thr Gly Cys Pro Gly Arg

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _09/037,667_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length
Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence.

8 _____ Skipped Sequences (OLD RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: -
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ Use of n's or **Xaa's** (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

11 _____ Use of <213>Organism (NEW RULES)
Sequence(s) _____ are missing this mandatory field or its response.

12 _____ Use of <220>Feature (NEW RULES)
Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

AKS-Biotechnology Systems Branch- 5/15/99